



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,016A

DATE: 02/14/2002

TIME: 10:12:44

Input Set : A:\A34157.txt

Output Set: N:\CRF3\02142002\I744016A.raw

ENTERED

3 <110> APPLICANT: Dr. Voelkel, Helge
 5 <120> TITLE OF INVENTION: Method for screening of modulators of calcineurin
 6 activity
 8 <130> FILE REFERENCE: A34157PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/744,016A
 C--> 11 <141> CURRENT FILING DATE: 2001-10-03
 13 <150> PRIOR APPLICATION NUMBER: EP98113876
 14 <151> PRIOR FILING DATE: 1998-07-22
 16 <160> NUMBER OF SEQ ID NOS: 35
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 5184
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
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 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (662)..(1123)
 28 <223> OTHER INFORMATION: copper/zinc superoxide dismutase
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1124)..(1849)
 33 <223> OTHER INFORMATION: enhanced green fluorescent protein
 35 <400> SEQUENCE: 1
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 38 cgttacataa cttacggttaa atggcccgcg tggctgaccg cccaacgacc cccgcccatt 120
 40 gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc attgacgtca 180
 42 atgggtggag tattttacgtt aaactgcca cttggcagta catcaagtgt atcatatgcc 240
 44 aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt atgcccagta 300
 46 catgacctta tgggactttc ctacttggca gtacatctac gtattagtca tcgctattac 360
 48 catggtgatg cgggttttggc agtacatcaa tgggcgtgga tagcggtttg actcacgggg 420
 50 atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc aaaatcaacg 480
 52 ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg gtaggcgtgt 540
 54 acggtgggag gtctatataa gcagagctgg tttagtgaac cgtcagatcc gctagcgcta 600
 56 ccggactcag atctcgagct caagcttcga attctgcagt cgacgggtacc gcgggcccgc 660
 58 c atg gcg acg aag gcc gtg tgc gtg ctg aag ggc gac ggc cca gtg cag 709
 59 Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln
 60 1 5 10 15
 62 ggc atc atc aat ttc gag cag aag gaa agt aat gga cca gtg aag gtg 757
 63 Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val
 64 20 25 30
 66 tgg gga agc att aaa gga ctg act gaa ggc ctg cat gga ttc cat gtt 805
 67 Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val
 68 35 40 45

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*Need
re-run
for
first page*

70	cat	gag	ttt	gga	gat	aat	aca	gca	ggc	tgt	acc	agt	gca	ggt	cct	cac	853
71	His	Glu	Phe	Gly	Asp	Asn	Thr	Ala	Gly	Cys	Thr	Ser	Ala	Gly	Pro	His	
72		50					55					60					
74	ttt	aat	cct	cta	tcc	aga	aaa	cac	ggg	ggg	cca	aag	gat	gaa	gag	agg	901
75	Phe	Asn	Pro	Leu	Ser	Arg	Lys	His	Gly	Gly	Pro	Lys	Asp	Glu	Glu	Arg	
76	65					70					75					80	
78	cat	gtt	gga	gac	ttg	ggc	aat	gtg	act	gct	gac	aaa	gat	ggt	gtg	gcc	949
79	His	Val	Gly	Asp	Leu	Gly	Asn	Val	Thr	Ala	Asp	Lys	Asp	Gly	Val	Ala	
80					85					90					95		
82	gat	gtg	tct	att	gaa	gat	tct	gtg	atc	tca	ctc	tca	gga	gac	cat	tgc	997
83	Asp	Val	Ser	Ile	Glu	Asp	Ser	Val	Ile	Ser	Leu	Ser	Gly	Asp	His	Cys	
84				100					105					110			
86	atc	att	ggc	cgc	aca	ctg	gtg	gtc	cat	gaa	aaa	gca	gat	gac	ttg	ggc	1045
87	Ile	Ile	Gly	Arg	Thr	Leu	Val	Val	His	Glu	Lys	Ala	Asp	Asp	Leu	Gly	
88			115					120						125			
90	aaa	ggt	gga	aat	gaa	gaa	agt	aca	aag	aca	gga	aac	gct	gga	agt	cgt	1093
91	Lys	Gly	Gly	Asn	Glu	Glu	Ser	Thr	Lys	Thr	Gly	Asn	Ala	Gly	Ser	Arg	
92		130					135					140					
94	ttg	gct	tgt	ggt	gta	att	ggg	atc	gcc	caa	acc	acc	atg	gtg	agc	aag	1141
95	Leu	Ala	Cys	Gly	Val	Ile	Gly	Ile	Ala	Gln	Thr	Thr	Met	Val	Ser	Lys	
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98	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	gag	ctg	gac	1189
99	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	
100				165					170					175			
102	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	ggc	gag	ggc	1237
103	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	
104				180					185					190			
106	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	acc	acc	ggc	1285
107	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	
108			195					200					205				
110	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	acc	tac	ggc	1333
111	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	
112		210					215						220				
114	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	1381
115	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	
116	225					230					235				240		
118	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	1429
119	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	
120				245						250				255			
122	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	1477
123	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	
124			260						265					270			
126	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	1525
127	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	
128			275				280						285				
130	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	1573
131	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	
132		290					295					300					
134	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	1621

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135 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
136 305 310 315 320
138 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 1669
139 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
140 325 330 335
142 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 1717
143 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
144 340 345 350
146 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 1765
147 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
148 355 360 365
150 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 1813
151 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
152 370 375 380
154 ggg atc act ctc ggc atg gac gag ctg tac aag taa agcggccgcg 1859
155 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
156 385 390 395
158 actctagatc ataatcagcc ataccacatt tgtagagggtt ttacttgcctt taaaaaacct 1919
160 cccacacctc ccctgaacc tgaaacataa aatgaatgca attgttggtt ttaacttggt 1979
162 tattgcagct tataatgggtt acaaataaag caatagcatc acaaatttca caaataaagc 2039
164 attttttttca ctgcattcta gttgtgggtt gtccaaactc atcaatgtat ctttaaggcgt 2099
166 aaattgtaag cgtaaatatt ttgttaaat tgcggttaaa tttttgttaa atcagctcat 2159
168 tttttaacca ataggccgaa atcggaacaaa tcccttataa atcaaaaagaa tagaccgaga 2219
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210 ccatcatggc tgatgcaatg cggcggtgc atacgttga tccggctacc tgcccattcg 3479
212 accaccaagc gaaacatcgc atcgagcgag cacgtactcg gatggaagcc ggtcttgctg 3539
214 atcaggatga tctggacgaa gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc 3599
216 tcaaggcgag catgcccagc ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc 3659
218 cgaatatcat ggtggaaaat ggccgctttt ctggattcat cgactgtggc cggctgggtg 3719
220 tggcggaccg ctatcaggac atagcgttgg ctaccgctga tattgctgaa gagcttggcg 3779

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222 gcgaatgggc tgaccgcttc ctctgtcttt acggtatcgc cgctcccgat tcgcagcgca 3839
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226 cgaccaagcg acgcccaccc tgccatcacg agatttcgat tccaccgccg ccttctatga 3959
228 aaggttgggc ttccggaatcg ttttcgggga cgccggctgg atgacccctc agcgcgggga 4019
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236 accgagacct cattggggcc aatacgcccg cgtttcttcc ttttccccac cccaccccc 4259
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240 ctcaggttac tcatatatac ttttagattga tttaaaactt catttttaat ttaaaaggat 4379
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244 ccaactgagcg tcagaccccg tagaaaagat caaaggatct tcttgagatc ctttttttct 4499
246 gcgcgtaatc tgcgtcttgc aaacaaaaaa accaccgcta ccagcgggtg tttgtttgcc 4559
248 ggatcaagag ctaccaactc tttttccgaa ggtaactggc ttcagcagag cgcagatacc 4619
250 aaatactgtc cttctagtgt agcogtagtt agggccaccac ttcaagaact ctgtagcacc 4679
252 gcctacatac ctgcgtctgc taatcctgtt accagtgggt gctgccagtg gcgataagtc 4739
254 gtgtcttacc gggttggact caagacgata gttaccggat aaggcgcagc ggtcgggctg 4799
256 aacggggggg tcgtgcacac agcccagctt ggagcgaacg acctacaccg aactgagata 4859
258 cctacagcgt gagctatgag aaagcgccac gcttcccga gggagaaaagg cggacaggta 4919
260 tccggttaagc ggcagggtcg gaacaggaga gcgcacgagg gagcttccag ggggaaacgc 4979
262 ctggtatctt tatagtctcg tcgggtttcg ccacctctga cttgagcgtc gatttttgtg 5039
264 atgctcgtca ggggggcgga gcctatggaa aaacgccagc aacgcggcct ttttacggtt 5099
266 cctggccttt tgctggcctt ttgctcacat gttctttcct gcgttatccc ctgattctgt 5159
268 ggataaccgt attaccgcca tgcatt 5184
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272 <211> LENGTH: 154
273 <212> TYPE: PRT
274 <213> ORGANISM: Homo sapiens
276 <400> SEQUENCE: 2
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278 1 5 10 15
280 Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val
281 20 25 30
283 Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val
284 35 40 45
286 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His
287 50 55 60
289 Phe Asn Pro Leu Ser Arg Lys His Gly Gly Pro Lys Asp Glu Glu Arg
290 65 70 75 80
292 His Val Gly Asp Leu Gly Asn Val Thr Ala Asp Lys Asp Gly Val Ala
293 85 90 95
295 Asp Val Ser Ile Glu Asp Ser Val Ile Ser Leu Ser Gly Asp His Cys
296 100 105 110
298 Ile Ile Gly Arg Thr Leu Val Val His Glu Lys Ala Asp Asp Leu Gly
299 115 120 125
301 Lys Gly Gly Asn Glu Glu Ser Thr Lys Thr Gly Asn Ala Gly Ser Arg
302 130 135 140
304 Leu Ala Cys Gly Val Ile Gly Ile Ala Gln
305 145 150

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309 <211> LENGTH: 241
310 <212> TYPE: PRT
311 <213> ORGANISM: Homo sapiens
313 <400> SEQUENCE: 3
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315 1 5 10 15
317 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
318 20 25 30
320 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
321 35 40 45
323 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
324 50 55 60
326 Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
327 65 70 75 80
329 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
330 85 90 95
332 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
333 100 105 110
335 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
336 115 120 125
338 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
339 130 135 140
341 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
342 145 150 155 160
344 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
345 165 170 175
347 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
348 180 185 190
350 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
351 195 200 205
353 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
354 210 215 220
356 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
357 225 230 235 240
359 Lys

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363 <210> SEQ ID NO: 4
364 <211> LENGTH: 6268
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366 <213> ORGANISM: Homo sapiens
368 <220> FEATURE:
369 <221> NAME/KEY: CDS
370 <222> LOCATION: (613)..(1329)
371 <223> OTHER INFORMATION: enhanced green fluorescent protein
373 <220> FEATURE:
374 <221> NAME/KEY: CDS
375 <222> LOCATION: (1330)..(2859)
376 <223> OTHER INFORMATION: calcineurin A alpha
378 <400> SEQUENCE: 4

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2323 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 17, CDS
LOCATION:115..1713
L:2464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2484 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2504 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:2928 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2932 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2936 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2940 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2944 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2948 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2952 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2956 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2960 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2964 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:2968 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:3439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3443 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3447 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3451 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3455 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3467 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3471 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:3475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3479 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:3756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:3777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25

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L:3780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:4005 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:4045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:4325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:4514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:4518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:4522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:4526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:4530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:4534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29